



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Zsebo, Krisztina M.  
Bosselman, Robert A.  
Suggs, Sidney V.  
Martin, Francis H.
- (ii) TITLE OF INVENTION: Stem Cell Factor
- (iii) NUMBER OF SEQUENCES: 104
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
(B) STREET: 6300 Sears Tower, 233 South Wacker Drive  
(C) CITY: Chicago  
(D) STATE: Illinois  
(E) COUNTRY: United States of America  
(F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/449,649  
(B) FILING DATE: 24-MAY-1995  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/982,255  
(B) FILING DATE: 25-NOV-1992
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/589,701  
(B) FILING DATE: 01-OCT-1990
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/573,616  
(B) FILING DATE: 24-AUG-1990
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/537,198  
(B) FILING DATE: 11-JUN-1990
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/422,383  
(B) FILING DATE: 16-OCT-1989
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Clough, David W.  
(B) REGISTRATION NUMBER: 36,107  
(C) REFERENCE/DOCKET NUMBER: 01017/32953
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 312/474-6300  
(B) TELEFAX: 312/474-0448  
(C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu	Glu	Ile	Cys	Arg	Asn	Pro	Val	Thr	Asp	Asn	Val	Lys	Asp	Ile	Thr	
1				5					10					15		
Lys	Leu	Val	Ala	Asn	Leu	Pro	Asn	Asp	Tyr	Met	Ile	Thr	Leu	Asn	Tyr	
			20					25					30			
Val	Ala	Gly	Met	Asp	Val	Leu	Pro	Ser	His	Cys	Trp	Leu	Arg	Asp	Met	
		35					40					45				
Val	Thr	His	Leu	Ser	Val	Ser	Leu	Thr	Thr	Leu	Leu	Asp	Lys	Phe	Ser	
	50					55					60					
Asn	Ile	Ser	Glu	Gly	Leu	Ser	Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Gly	
65					70					75				80		
Lys	Ile	Val	Asp	Asp	Leu	Val	Ala	Cys	Met	Glu	Glu	Asn	Ala	Pro	Lys	
			85						90					95		
Asn	Val	Lys	Glu	Ser	Leu	Lys	Lys	Pro	Glu	Thr	Arg	Asn	Phe	Thr	Pro	
			100					105					110			
Glu	Glu	Phe	Phe	Ser	Ile	Phe	Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	
		115					120					125				
Phe	Met	Val	Ala	Ser	Asp	Thr	Ser	Asp	Cys	Val	Leu	Ser	Ser	Thr	Leu	
	130					135					140					
Gly	Pro	Glu	Lys	Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	
145					150					155					160	
Pro	Pro	Val	Ala	Ala												
				165												

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /mod\_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACRTTYTTNG GNGCRTTYTC YTCCAT

26

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 12 & 15
- (D) OTHER INFORMATION: /mod\_base= Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AARAAATCYT CNGGNGTRAA RTT

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTATCNGGYT TYTT

14

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGARGARA AYGCCCCCAA RAAYGT

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCNAAYGAYT AYATGWTMAC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGNGGNARCA TRAANGGYTT 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACCAKAARAT CTTYAAANCG ATC 23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTATTTTCAA TAGATCCATT GA 22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAACTATGT CGCC 14

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:  
 GTAGTCAAGC TGACTGATAA G 21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
 TAACCAACAA TGACTAGGCA A 21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:  
 TTCCAGAGTC AGTGTC 16

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
 GCGAAGCTTG CCTTTCCTTA TGAAGAAGA 29

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
 GCGCCGCGGT TACGGTGGTA ACATGAAGGG CTTGTGA 38

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATAAATGCA AGTGATAATC C

21

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGGTCGACC CGCGGAACTT TAAGTCCATG CAACAC

36

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CACCCGCGGT TATGCAACAG GGGGTAACAT AAATGG

36

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACCCGCGGT TAGGCTGCAA CAGGGGGTAA CATAAA

36

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
CTTAATGTTG AAGAAACC 18

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
GATGGTAGTA CAATTGTCAG AC 22

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
GTCTGACAAT TGTACTACCA TC 22

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
CAATTTAGTG ACGTCTTTTA CA 22

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:  
TTAGATGAGT TTTCTTTCAC GCAC 24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAATCATTCA AGAGCCCAGA ACCC

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACATCCATC CCGGGGAC

18

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTGGCAATAT TTTAAGTCTC AAGAAGACC

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCGCCGCGGC TCCTATAGGT GCTAATTGG

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:  
CCTCACC ACT GTTTGTGCTG GATCGCA 27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:  
GGTGTCTAGA CTTGTGTCTT CTCATAAGG A 31

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:  
CCCCCCHGG 10

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:  
TTTTTTTTTT TTTTTTTTGG 20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  
TTTTTTTTTT TTTTTTTTAG 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTTTTTTTTT TTTTTTTTCG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTCGGCCGAT CAGGCCCCCC CCCC

24

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGCCGGATAG GCCTCACNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGCCGGATAG GCCTCAC

17

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(660..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(720..773, 1184..1246, 2053..2223, 2837..2993, 3692..3774)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAAGTATCTT TCTATTGGCG AAGGACATGT TTTCCCATAA GTGGTAAACA AACTGTCTGC	60
ACATAATAAT TATCTTGCTG CCGTAAAGAT TAGGTTAAAT TCTGCCTTCG ATCTAAAAAC	120
ACACCCTTCT GTCAATCCGA GGAGCAGTGT GCTAGTCTAG AGGTCTAAAT GAAGGCTCCT	180
TTCACGGTTG TATTTCTGCT CCCCAAATTG TCCACATTTA AAAGGAGAGT GCTTCTTTTC	240
AGCCTTAGGC TCTGAATTTT ATGCATTCCT CCATTTTCCG AGGTCCCCC CAAGTGATAA	300
TTCTGTTACA CGTTGCTACA AGTTCATCCC TAATTGCCGT CAAGAACTG ACTGTAGAAG	360
GCTTACCACA GACGTTGTAA CCGACAGTAA AGCCATTGAA AGAGTAATTC AAACAGGATG	420
GAAGCCAGGA GTATTTTGTG GCTGTTGCTC TTTTCTTTT CAGTTTGGTG AGAGCAGCTT	480
GAATGCTTAA CATTTAAGCC ATCAGCTTAA AACAAAACAA AACAAAACAA AAAAAAACC	540
CGCTCTGGCA TATTTGCACT TAACACATAC GGTATAAGGT GTTACTGGTT TGCATAGTTC	600
TGGATTTTTT TTTTTTAAAA ACTGATGGAC ACCAAGAAAT GTTTCTGTTC TTTGTTTAG	659
ACT TGG ATT ATC ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT	707
Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	
-20 -15 -10 -5	
CTC GTC AAA ACT CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA	755
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	
1 5 10	
AAA GAC ATT ACA AAA CTG GTAAGTAAAG AATGATTTTG GCATCTATAA	803
Lys Asp Ile Thr Lys Leu	
15	
GTCTTCCCTG TGCTTGCTGA CCACATAGGT TCAGGGCACT CCCGACAGGA GTTCCCAGCT	863
TTCTAAGATA AGGAATCACT GTACGAGTCT GAAGTGCTTC TTCTGGGCAA ATGGGAGATG	923

CTTAGGTCAT GGAGGGTTTA TCTGTATAAC TGGCCCTTTG CACACCAACA AAGTGA CTGA	983
CTGGCTTTTG CCTGTTACCT ACTGTCTCCA GTCCTGGGCA TGGTATATAC TTAGGCACCC	1043
AAGATTGGAT TTACAACTCA AGCATTATAT ATTGGACAAC ACGGGGTATG AGATATTAAT	1103
GATATGTCAG GTTGGATGGA TGAGTTTTCT CAAGAAATTC TCTTGATTTT ACTCACGTTT	1163
TCATTTCTTG GTCTCTGTAG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA	1213
Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	
20 25	
ACC CTC AAC TAT GTC GCC GGG ATG GAT GTT TTG GTATGTAGTC CACACACTTC	1266
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu	
30 35	
TGAGTTGCCT TTTAGTAGCT AATGGGTGAC CTGTGCTTAT TCACATTGAA GACATTATTT	1326
GCTCTTTGTC GTTTTTAGAT GTTGACCTAT AATTTTTCCT TCAAGCTGCT GCTAAGATTA	1386
TCAGTGAGCA TTTCAGTATG TGTTTTAAGC CTA CTCATTA AAAGGAAATG GCTCATCTTA	1446
GACGTAGCAA CCGATGTTAA TTTTTCCTCA GGCATCTCTC AGAGGGACTT GAATGTTAAA	1506
ATCATGTTAA ATTTCTCCT TGGCTATGTT ATTTCTCATG GCTATGTTAT TCCTATTCGT	1566
ATTTCAITTA AAGGGACGGA ATATTTATTG TATTTCTGAA CTTTTTCAGG CATGCATCCG	1626
GGTCTTTGAA TAAAACACTA AGACTCCTTC TAGTAATGTT TGTAATCCTG TCTGTATCGA	1686
ATGTCTTTGA AAACGCAGTG ACTAAGCCAT AAATAATCTT CCACAGAACG TCCAGTG GTT	1746
CATGAAC TTT GTATGTGGGG GTGGGGCAAG AATTGTCTCA CTATTGGTCA AGGAAGAGAA	1806
GGTAAGGTAT GCAAGGGTGG TTTAATCTTC TTCCGTGGAA GGACAAAATC ATCTATCATT	1866
TCCTCTGATC TCTATGCATT TGTTTGTTTT GAACTGAATC TGACTTGAGC AAGAGTTGGC	1926
GTCCTGTGTT CTGAGGAAAC TCTTTGTCCT GCAGTCAGTG ACTAAAAGTG CTGAGAGATC	1986
TGAAGAGCAC TCTGAATCTG CCATATTTTT AATAGATGCT TTGTCTTCTC TTTGAATTTT	2046
TTCCAG CCT AGT CAT TGT TGG TTA CGA GAT ATG GTA ACA CAC TTA TCA	2094
Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser	
40 45 50	
GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC	2142
Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly	
55 60 65	
TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG AAA ATA GTG GAT GAC	2190
Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp	
70 75 80 85	
CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG GTA ACTTGGT ATTCATCAGA	2243
Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
90 95	
ATTATTTTTT TTATACTGAG CTCATGATGA GCAATTCACA ACCACTTGTA ATTCCAGCTC	2303
CAGAGGACAT TATCCCCTCT TTGGATGCCA TAGGAATCTG CTCTCAAATA TG TAGATACC	2363
ACCTCTGCCA CCTCAGCACA TACATACACA TAATTAAAAA ATAGAAACAT TAAAGGAGTT	2423

CCAATCAATC CTTATTCTTT TCTGTATTCA GSTATGCCAG ATGTAAATTC TAGGAATATG	2483
TTTTAAAGGC TAATTCTTAT TTTGTAATAA GCAGCTTTAA AATTCTTAAT TGTTTTTTTCG	2543
GGTCACTTTA TTGTCCTATT GCCACGACAT TGTCTGTGCC CATTGTCTGT TATTCCTTCT	2603
GTTTTGTTTA TTGTTCCCTA GTTACTTTGA TCATGAGATT GACCTGTTAC CCGTTGTTAT	2663
TCTCTGTAGC CATTTTGAGT TGTGTCTATT AGAACAGCTG TTAAATTACT TGAATCATTG	2723
AGGACATAGT CAATAATCTA TTATGCTGAT CCAGTCAAGT CTATGAGTTA TTTGAAAAC	2783
AGAATCTTTG TTAATTATTT GTTTGCTTGT TTGTTTGT TTATTATTGTC TAG AAT	2839
	Asn
GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT GAA	2887
Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu	
100 105 110	
GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC TTC	2935
Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
115 120 125	
ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA GGT	2983
Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu Gly	
130 135 140 145	
CCT GAG AAA G GTAAGGCTTT TAAGCATTTT TTGTTTAAAT GTACATAGAA	3033
Pro Glu Lys	
AGCCTGAACT TCTGTAAGCC TCTACTGCTG AATCAACTAA ATGTGTTGCT GTAGAAAGAA	3093
CGTGTGGGTT TTTCTGATAA AAACAAAAAG CAAATATCAA TGACTACCAA TGATTATTAT	3153
CTAGCTTGAG AGATATGCCC TAAGACAGCG ATTCTCGATA TTTCTAAATT AAAGAATTGT	3213
GTGATGGTGG CTCACATATT TTCTAACTGT GATATTTGCC AGGAGAGTAG AATAATGTTA	3273
TTCTTCATCC CCAGAATTCC TAAGATTTCA CGTCTCATGT CTTTTCCATA AGGTTCAAAC	3333
TCTGAGACTT GAGTTCTGAG CCTCAGCAGG TCATTCTGAA TCCCCACTCT CCCCAGAGCTG	3393
GGTCCCTATG GGGGAACTAA CTTCAATTGCT TTCTTTTAAA ACATGACGAG TTACCAACAG	3453
CTCCTCGCTA TTATAAACAT GTTCCTAAGC ATGTCTGTGC ATGCAATAAG CCTTCACTCT	3513
ACAAGACAGT TATGGTGTAT CGCTTGACAA AACTGAGCAG CCAAGCTGAG TATGAAATAA	3573
TAATCTAGAC TTGGGAGGCA GACCCAGCAC CTACTGTGAT ATTGCACTTC GCCTTTGGGG	3633
GACTCTATGA TTCAAAAGTT CACCATGTAA CACTGACACA TTATTGCTTT CTATTTAG AT	3693
	Asp
TCC AGA GTC AGT GTC AGA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC	3741
Ser Arg Val Ser Val Arg Lys Pro Phe Met Leu Pro Pro Val Ala Ala	
150 155 160 165	
AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGTAAGTACA CATATCTGAT	3794
Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn	
170 175	

TTACTGCATG CATGGCTCCA AGTATCCTCT ATAGGAGTGT TGCATGGACT TAAAGTTTAT	3854
AAATCACTAC TAATAATGCT GTTCTGTCAC TGTATTTCCT TGTATGGGCT TCCTGACAAT	3914
TAAATATCTG GTTTGTAGAA TCGGATCTCC TTAGAGGTTA AGATGACCAT GACAAAATTA	3974
GGCCAATCAA CTTTCTGCGA AGGTTATTTT AAATAAGGCA CGAAATTAAT TGAAGGAAAA	4034
AAAAATACAA GCAAGGCCTT ATTTTGAATC ATGGTAGGCT TAAAATAGAC TTTGTGGAGA	4094
ATGTCCCTGA TCAAAGTGGA GTTTTCAGAT TTCAAGTGCA TGTGCTAACT CTCCACAATG	4154
TCAAGGCTAT TTTCAGTTTT GTGTCTCCAT ATTTACTACT GCATGTTTGG AAATTTGCTG	4214
ATGCTGTTAG ATTACCTAAG AATGTATGTT GAAGAAGAAT GGACTTCTTT CCCTAAAATT	4274
TCTGTCCTCT TTGCCCAAGA ACCCACGTTT CTGGAAGACT ATCTTATTTT CATGTCTGTG	4334
CAATGATCAT TATAAAGATT ATTGAATATA CTGGAATAC TCTGGTTTCT GTTTTTACAG	4394
ATTCATAATA GCTTATTCAG TCTTTAAAGA AAGTTCTCTG AAGTCCATGC TTTAGAATGT	4454
TTCTCTATCA AAAGTTGACC TGGACCTTAA ATAAAGCTAT ATTTAGTCTT TTTATCCCTG	4514
AAAAATATAT TTCACAGTGT AGACATTTGA TATACATCTA AGGGAAGGAT GCTGCCAGAA	4574
TGCTCGGGCT GGCAGTCTAC AAAGTCCACT GCTCTCAGGA TGGACTTCTG AAAGCGGAAA	4634
TTGTGAACTG CATGCATATA ACATATCAGA TCCTCGAGC	4673

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro	-20	-15	-10	-5
Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val	1	5	10	
Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile	15	20	25	
Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp	30	35	40	
Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu	45	50	55	60
Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile	65	70	75	
Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu	80	85	90	

Asn Ala Pro Lys Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg  
           95                          100                          105  
 Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp  
       110                          115                          120  
 Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu  
   125                          130                          135                          140  
 Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg Val Ser Val Arg Lys  
           145                          150                          155  
 Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser  
           160                          165                          170  
 Ser Ser Ser Asn  
       175

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..844

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 101..844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGGATCGCA GCGCTGCCTT TCCTT ATG AAG AAG ACA CAA ACT TGG ATT ATC	52
Met Lys Lys Thr Gln Thr Trp Ile Ile	
-25 -20	
ACT TGC ATT TAT CTT CAA CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT	100
Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys Thr	
-15 -10 -5	
CAG GAG ATC TGC AGG AAT CCT GTG ACT GAT AAT GTA AAA GAC ATT ACA	148
Gln Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr	
1 5 10 15	
AAA CTG GTG GCG AAT CTT CCA AAT GAC TAT ATG ATA ACC CTC AAC TAT	196
Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr	
20 25 30	
GTC GCC GGG ATG GAT GTT TTG CCT AGT CAT TGT TGG TTA CGA GAT ATG	244
Val Ala Gly Met Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met	
35 40 45	
GTA ACA CAC TTA TCA GTC AGC TTG ACT ACT CTT CTG GAC AAG TTT TCA	292
Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu Asp Lys Phe Ser	
50 55 60	

AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GGG	340
Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Gly	
65 70 75 80	
AAA ATA GTG GAT GAC CTC GTG GCA TGT ATG GAA GAA AAT GCA CCT AAG	388
Lys Ile Val Asp Asp Leu Val Ala Cys Met Glu Glu Asn Ala Pro Lys	
85 90 95	
AAT GTA AAA GAA TCA CTG AAG AAG CCA GAA ACT AGA AAC TTT ACT CCT	436
Asn Val Lys Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro	
100 105 110	
GAA GAA TTC TTT AGT ATT TTC AAT AGA TCC ATT GAT GCC TTC AAG GAC	484
Glu Glu Phe Phe Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp	
115 120 125	
TTC ATG GTG GCA TCT GAC ACT AGT GAT TGT GTG CTC TCT TCA ACA TTA	532
Phe Met Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Ser Thr Leu	
130 135 140	
GGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA	580
Gly Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu	
145 150 155 160	
CCC CCT GTT GCA GCC AGT TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT	628
Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn	
165 170 175	
AGG AAA GCC GCA AAG TCC CCT GAA GAC CCA GGC CTA CAA TGG ACA GCA	676
Arg Lys Ala Ala Lys Ser Pro Glu Asp Pro Gly Leu Gln Trp Thr Ala	
180 185 190	
ATG GCA CTG CCG GCT CTC ATT TCG CTT GTA ATT GGC TTT GCT TTT GGA	724
Met Ala Leu Pro Ala Leu Ile Ser Leu Val Ile Gly Phe Ala Phe Gly	
195 200 205	
GCC TTA TAC TGG AAG AAG AAA CAG TCA AGT CTT ACA AGG GCA GTT GAA	772
Ala Leu Tyr Trp Lys Lys Lys Gln Ser Ser Leu Thr Arg Ala Val Glu	
210 215 220	
AAT ATA CAG ATT AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA CAG	820
Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Gln	
225 230 235 240	
AAA GAG AGA GAG TTT CAA GAG GTG TAATT	849
Lys Glu Arg Glu Phe Gln Glu Val	
245	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu
-25 -20 -15 -10



Leu Leu Phe Asn Pro Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro  
                     -5                    1                    5  
 Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro  
                     10                    15                    20  
 Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu  
                     25                    30                    35  
 Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser Val Ser  
                     40                    45                    50                    55  
 Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
                     60                    65                    70  
 Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val  
                     75                    80                    85  
 Ala Cys Met Glu Glu Asn Ala Pro Lys Asn Val Lys Glu Ser Leu Lys  
                     90                    95                    100  
 Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe  
                     105                    110                    115  
 Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr  
                     120                    125                    130                    135  
 Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg  
                     140                    145                    150  
 Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
                     155                    160                    165  
 Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ser Pro  
                     170                    175                    180  
 Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile  
                     185                    190                    195  
 Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys  
                     200                    205                    210                    215  
 Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
                     220                    225                    230  
 Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
                     235                    240                    245

Val

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3807 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(905..1018, 1914..1976, 2572..2742, 3152

..3307, 3513..3595)

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: join(965..1018, 1914..1976, 2572..2742, 3152  
..3307, 3513..3595)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACAAGTGAG TAGGGCGCGC CCGGGAGCTC CCAGGCTCTC CAGGAAAAAT CGCGCCCGGT	60
GCCCCGGGGA AGCCGGCGCT CCCTGGGACT TGCAGCTGGG GCGTGCAGGG CTGTGCCTGC	120
CGGGTGAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT ACAGTGTAAT	180
AAGGAAAAAT AAGTCATGCA TAAAGCAAC TATAATACAT AATAGAAAAT GTTATTTTCA	240
AGCCGATGTG TAGGTTATGT GTGTTGAGA GAGAGAGAGA GAAGACAGAT TACTTTCTGC	300
TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT GGCTAAAAAG	360
CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGAATTCTC TTAGGTCTAA	420
AAATATACAT CTCTCTCACT TTAACCTGGT GTGCTATTGT AGATTATTGG ATTAAAGCAC	480
TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA AATAAGATGT	540
TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA AGATACCCTA	600
AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG GGAAATTGGC	660
TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT TCAAAATGGA	720
TTTTAACTAA AAGCTTTTAA AAACCTTGGT GAGCATAGCT TGAATGCGTA ATATTTAATT	780
GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTTGT GCATCAAGGC ATTAGATGTT	840
AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT CTGTTTTCAT	900
TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT	949
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn	
-20 -15 -10	
CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT	997
Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn	
-5 1 5 10	
GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC CGTGCTGTGT	1048
Val Lys Asp Val Thr Lys Leu	
15	
AAAAAAGAGC TGTGGCTCTT TTTCTGTGCT TTGTTGATAA AAGATTTAGA TTTTCTTGC	1108
CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT AAAGGGTTTA	1168
TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA ACTGGCTAGT	1228
TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC ATAGGCAGTG	1288
AAGGACCTTG GAGAGTTGCG TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT CCCATAATC	1348
TCTCCAGTGG GTTTCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA CTCTTCTTTA	1408

AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA GCAGGAAGAC	1468
CCTGTACACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG ATTCATTGCC	1528
CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTACATTG AACTCTTCCC TCAGCGAAAG	1588
CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC AGATCATGTT	1648
TCCAAAACCTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC TAAAAGATCT	1708
GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTTGATTA CAGAGGGAAA TCAAGGATTA	1768
AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAAGC ACAACAGTTT	1828
TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA ATTTTCTTAT	1888
GGAATTTTTT TTTTGTCTC TG TAG GTG GCA AAT CTT CCA AAA GAC TAC ATG	1940
Val Ala Asn Leu Pro Lys Asp Tyr Met	20 25
ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG GTATGTAAAC	1986
Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	30 35
TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC ATATTGAGAT	2046
AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA TTTATCTTTG	2106
GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCCTGTT ACAAGAGTCC CTCCTCTAT	2166
TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTTCTGTGTA CAATAACCCC	2226
TGTCCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC TGGCCAGGCA	2286
CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG ATCATTGAG	2346
GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC TAAAAATAAA	2406
AAAGTAGCCA GGCATGGTGG CAGGCACTTG TAATCTGAGC TACTCGAGAG GCTGAGGCAG	2466
GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT TTATGGCACT	2526
TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA AGT CAT	2580
Pro Ser His	40
TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT	2628
Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp	45 50 55
CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC	2676
Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser	60 65 70
ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG	2724
Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu Cys Val	75 80 85 90
AAA GAA AAC TCA TCT AAG GTAACCTTGT GTTCATTGGG ATTATTTTTC	2772
Lys Glu Asn Ser Ser Lys	95
ATTACGCTTC TCTAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	2832

TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTTCAGA TGAGCAAAGA	2892
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC ATTCTTGTGT TCACTGCCCC	2952
AGATTCAACT TGTGATCCCA CTGGGATCAC TACCCTGCAT TACCAATCTG AATTACATAC	3012
GTTAAACAG CCATCTAAAA GTGCTAGTTG TAAGAGTCTA AATACTTGAA TCTTTGAGAG	3072
ACATATTTAT AGTCCATTAT CTTCACCTCA GTTAAGTCTG AAGACTATTT GAAAAATGTA	3132
ATCCTATTTT TTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC	3184
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro	
100 105	
AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT	3232
Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile	
110 115 120	
GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG	3280
Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val	
125 130 135	
GTT TCT TCA ACA TTA AGT CCT GAG AAA GGTAAGACAT GTAAGCATTT	3327
Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CCAGTTCAAA TGTAACAAC AAACCTAAAT CTTCCCTATG TAGTAAGAAT CTACCTCTGT	3387
GTTAAGCTGT AGCAAGATAC ATGCATGTAC GTCTAATAAA AAAGCAGATA TCAATAGCAC	3447
AGAAGAACT CTATAACTCA TACAAATCAC CATATAACAC TGACACATTA TTGCTTTCTA	3507
TTTAG ATT CCA GAG TCA GTG TCA CAA AAC CAT TTA TGT TAC CCC CTG	3554
Ile Pro Glu Ser Val Ser Gln Asn His Leu Cys Tyr Pro Leu	
150 155 160	
TTG CAG CCA GCT CCC TTA GGA ATG ACA GCA GTA GCA GTA ATAGTAAGTA	3603
Leu Gln Pro Ala Pro Leu Gly Met Thr Ala Val Ala Val	
165 170 175	
CATATATCTG ATTTAATGCA TGCATGGCTC CAATTAGCAC CTATAGGAGT ATTGCATGGG	3663
CTTTCAAGGA AACTTCTACA TTTATTATTA TTGATACTGT TCTGT TACTG TTATTCCTTT	3723
TATGGTCTTC TTGAGACTTA AGTTTGTAGA ATTAAATTTT CCTAGAGCTG GAGATAATGT	3783
TTAGAGAATT AGGCCAATAA ATTT	3807

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro
-20 -15 -10 -5



ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu 5 10 15	145
GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro 20 25 30	193
GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val 35 40 45 50	241
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile 55 60 65	289
TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile 70 75 80	337
GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu 85 90 95	385
AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu 100 105 110	433
TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val 115 120 125 130	481
GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro 135 140 145	529
GAG AAA GAT TCC AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro 150 155 160	577
GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGT AAG Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys 165 170 175	625
TAC ATA TAT CTG ATT TAATGCATGC ATGGCTCCAA TTAGCACCTA TAGGAGTATT Tyr Ile Tyr Leu Ile 180	680
GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG ATACTGTTCT GTTACTGTTA	740
TTCCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT AAATTTCCCT AGAGCTGGAG	800
ATAATGTTTA GAGAATTAGG	820

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

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Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu
-25          -20          -15          -10

Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg
          -5          1          5

Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro
          10          15          20

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu
          25          30          35

Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser
          40          45          50          55

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser
          60          65          70

Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val
          75          80          85

Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys
          90          95          100

Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe
          105          110          115

Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr
          120          125          130          135

Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg
          140          145          150

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser
          155          160          165

Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser Lys Tyr Ile Tyr Leu Ile
          170          175          180

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(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAGCTCCGAG CCCTCTCTGG CGCGCGAGGT ATTTCTGTCTG TNCCCGGGGG TGCCAGGTGA	60
GCCCCAGCGG ATCCGGGAGG GTAAGCTGGG ACTCCTCGCG AGCAGTAGCT GCAGGGTACC	120
AAGCTTCGCC CTCTGCGTCC CCGCGCCTTC GCGGTCTCCC GCCAGTGCAG GTCCGGGGGCC	180
CCCAGGCGAG CGGACAAGGT TGGCCTAATC TGCCAAACTT CTGGGGCATT TACCGTGCTC	240
TGGCCGCCCT CCCGATTCTT CCCTCCGCGC CTTTGCCTGC TTCTCGCCTA CCCCAGGGCTC	300
CGGAAGGGAA GGAGGCGTGT CCGGAGCAGG CGGGCGGGAA CTGTATAAAA GCGCCGCGCG	360
CTCAGCAGCC GGCTTCGCTC GCCGCCTCGC GCCGAGACTA GAAGCGCTGC GGGAAAGCAGG	420
GACAGTGGAG AGGGCGCTGC GCTCGGGCTA CCCAATGCGT GGAATATCTG CCGCCGCTGT	480
TCGTGCAATA TGCTGGAGCT CCAGAACAGC TAAACGGAGT CGCCACACCA CTGTTTGTGC	540
TGGATCGCAC CGCTGCCTTT CCTT ATG AAG AAG ACA CAA GTGAGTAGGG	589
Met Lys Lys Thr Gln	
-25	
CGCGCCCGGG AGCTCCCAGG CTCTCCAGGA AAAATCGCGC CCGGTGCCCC GGGGAAGCCG	649
GCGCTCCCTG GGACTTGCAG CTGGGGCGTG CAGGGCTGTG CCTGCCGGGT GAGACAAGAG	709
GATGCGGGGG AGGCCGGCGT GGTGTGTGAT CCCGAGCCGA GCCGNNTGAG CCAGGGAGAA	769
AAGGAGTGGG AGTACTGAGA GGGAGCCAGT GTCAAGTTTG GAGCCTCAGC AGTTAAGTTT	829
TGAGCTGTCA GTCGGAAACC GTAATTCCCG TCTGGTGGAA AGATTGGCTT TTNGNCCACG	889
GAATGTAAGT TATCACAGAT ACTACAAAGA TAAATCAGTT GCACAAGTTC TTGAAACTCT	949
ACAGTGTAAT AAGGAAAAAT AAGTCATGCA TAAAAGCAAC TATAATACAT AATAGAAAAAT	1009
GTTATTTTCA AGCCGATGTG TAGGTTATGT GTGTTCGAGA GAGAGAGAGA GAAGACAGAT	1069
TACTTTCTGC TAGGGTTCAA GAATGCCTTC CTGTTGGCTA AGGAAATATT TTCCTTAAGT	1129
GGCTAAAAAG CTGTGTTTCA AAATATTCTT TTGATGTCTC ACAAATTCAG TGGAATTCTC	1189
TTAGGTCTAA AAATATACAT CTCTCTCACT TTAAGTTGGT GTGCTATTGT AGATTATTGG	1249
ATTAAAGCAC TGCTCAGGGA TTATGCTGCT TCTTGCCAAG CAGTCTACAT TTAAAGTAGA	1309
AATAAGATGT TTCTTTTGGT GCCATAAGGT ATACATTTTA TGCATTCTCT AGTTTTTAGA	1369
AGATACCCTA AGGGCTAAGT CTTTAACATG CTGCTACAAG TTTATTCCTA ATTGCCATTG	1429
GGAAATTGGC TGAAGAAAGT TTTTAACAAA AGTTAACAAT ATTGTCATTG AGAGAATAAT	1489
TCAAAATGGA TTTTAACTAA AAGCTTTTAA AAAGTTTGGT GAGCATAGCT TGAATGCGTA	1549
ATATTTAATT GCATTTAAGC CAATAACATA TATTAGACTG GTCTTTTGT GCATCAAGGC	1609
ATTAGATGTT AAAAGTTTGA ATGATTACAG ATCTTAACTG ATGATCACCA AGCAATTTTT	1669
CTGTTTTTCAT TTAG ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG CTG CTC	1719
Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu Leu	
-20 -15 -10	



CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT CGT GTG	1767
Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg Val	
-5 1 5	
ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTAAGTAAGG AATGCTTTAC	1817
Thr Asn Asn Val Lys Asp Val Thr Lys Leu	
10 15	
CGTGTCTGTGT AAAAAAGAGC TGTGGCTCTT TTTCTGTGTC TTGTTGATAA AAGATTTAGA	1877
TTTTTCTTGC CCCAAAGTAA TGTTTTCTTA AAGTGGGGAA AGTAATCACT GGGTTACAAT	1937
AAAGGGTTTA TAGAAAGCAG GTAGTGAGAT ATTTAGGGTC ATGGATAATT TGTTGGTAAA	1997
ACTGGCTAGT TGCACACCAC TGCTGTGACT GCTTCTTTGC TGGTCTTCTC CCCATCCTTC	2057
ATAGGCAGTG AAGGACCTTG GAGAGTTCGC TGTGTGCTGA TGGGCTTGCC CCAGCTTGTT	2117
CCCCATAATC TCTCCAGTGG GTTTCCAGC ATGTTCTATT CCCCTTCACA TGTCTTCCTA	2177
CTCTTCTTTA AAAAGCCTAA CGAAAGGAAA TCTGAAATGG CTATTCTCCC AATTCAATCA	2237
GCAGGAAGAC CCTGTCACAT GTCAGTGGGT GTTTGCTCCT TCAGGGAACA TAGAGAGGTG	2297
ATTCATTGCC CACATGTTGA AGGGACTCAT CTCCCTGGTT TGTCACATTG AACTCTTCCC	2357
TCAGCGAAAG CATTTGCATT GCTTCCCGAA TTCCAAGATC ACAGGTGGAA GCTGAAATTC	2417
AGATCATGTT TCCAAAACCTC AGTAGGTTAT ACCTAGCCAG GCATAACTGA ATTTGGAGTC	2477
TAAAAGATCT GTATTATCAC TTTTTTATTT TGAAGGATGC CTTTTGATTA CAGAGGGAAA	2537
TCAAGGATTA AAAATCAATA TACATGTAAA TATTGAAATT CATTGGTAAC TTTAAAAGC	2597
ACAACAGTTT TGTGTGCTTT TCTCCAAAGC ACTACAAATA TGATTAATTG ATGTATAAGA	2657
ATTTTCTTAT GGAATTTTTT TTTTGTCTC TGTAG GTG GCA AAT CTT CCA AAA	2710
Val Ala Asn Leu Pro Lys	
20	
GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT TTG	2755
Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu	
25 30 35	
GTATGTAAAC TACATTTCTG AGTTTCATTT TAGTAGCTCA TAGAAGAAAT GGGATCATTC	2815
ATATTGAGAT AGTACACTAG CTGCTATTTA GGAGCTTGCT TATTGTCAGG ATTTGAAGAA	2875
TTTATCTTTG GAATTTGACT TGCAGGCTTT TTTTCCCCC TCTTCCTGTT ACAAGAGTCC	2935
CTCCTCCTAT TACAATAGTC CCTCCTCCTC CTGTCACACT AGTCCCTTCT CTCCTGTTA	2995
CAATAACCCC TGTCTCCTA TTACAACATT TTAAGTAATG TAATATTAAT TTTAAAAATC	3055
TGGCCAGGCA CGGTGGTTCA TGCTTGTAAT CCCAGCACAT TGGGAAGCTG AGACGGGTGG	3115
ATCATTTGAG GTCAGGAAGT TTGAGACAGC CTGGCCAACA TGGTGAAACT TCCTCTCTAC	3175
TAAAAATAAA AAAGTAGCCA GGCATGGTGG CAGGCACCTG TAATCTGAGC TACTCGAGAG	3235
GCTGAGGCAG GAGAATCACT TGAGTAACTA AAACGATAGC TTTGAAGAGT ACTCCGAGTT	3295
TTATGGCACT TACTTATTAA AATAGCTGTT TTGTCTCTTT TTTCATATCT TGCAG CCA	3353

AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC AGC TTG	3401
Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser Leu	
45 50 55	
ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG AGT AAT	3449
Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn	
60 65 70	
TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT GTG GAG	3497
Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val Glu	
75 80 85	
TGC GTG AAA GAA AAC TCA TCT AAG GTAACCTTTGT GTTCATTGGG ATTATTTTTC	3551
Cys Val Lys Glu Asn Ser Ser Lys	
90 95	
ATTACGCTTC TCTAAAAACC CATGCTTCTT GGTGCTGTTG GGGAAAATGA GGCACCTTTA	3611
TTTATGATAT TTTGATTGTA TAAACTTCAA ATTTAAAAAT CTTGTTCAGA TGAGCAAAGA	3671
AAACAAGTAT TTGCAGTTAT ACTGCAATAC TGAAGTGCAC TATTCTTGTG TTCACTGCCC	3731
CAGATTCAAC TTGTGATCCC ACTGGGATCA CTACCCTGCA TTACCAATCT GAATTACATA	3791
CGTTAAAACA GCCATCTAAA AGTGCTAGTT GTAAGAGTCT AAATACTTGA ATCTTTGAGA	3851
GACATATTTA TAGTCCATTA TCTTCACCTC AGTTAAGTCT GAAGACTATT TGAAAAATGT	3911
AATCCTATTT TTTCTTCTAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA	3961
Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu	
100 105	
CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC	4009
Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser	
110 115 120	
ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT	4057
Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys	
125 130 135	
GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA G GTAAGACATG TAAGCATTTT	4108
Val Val Ser Ser Thr Leu Ser Pro Glu Lys	
140 145	
CAGTTCAAAT GTAAACAACA AACTTAAATC TTCCCTATGT AGTAAGAATC TACCTCTGTG	4168
TTAAGCTGTA GCAAGATACA TGCATGTACG TCTAAAAAAA AGCAGATATC AATAGCACAG	4228
AAGAACTAA TGATTGTAGA TTTGTGGGCT CTATAACTCA TACAAATCAC CATATAACAC	4288
TGACACATTA TTGCTTTCTA TTTAG AT TCC AGA GTC AGT GTC ACA AAA CCA	4339
Asp Ser Arg Val Ser Val Thr Lys Pro	
150 155	
TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT GAC AGC AGT	4387
Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser	
160 165 170	

AGC AGT AAT A GTAAGTACAT ATATCTGATT TAATGCATGC ATGGCTCCAA Ser Ser Asn 175	4437
TTAGCACCTA TAGGAGTATT GCATGGGCTT TCAAGGAAAC TTCTACATTT ATTATTATTG	4497
ATACTGTTCT GTTACTGTTA TTCCTTTTAT GGTCTTCTTG AGACTTAAGT TTGTAGAATT	4557
AAATTTCCCT AGAGCTGGAG ATAATGTTTA GAGAATTAGG CCAATAAATT TTCTGCTGAG	4617
GTTATTTTAA ATAAGACATA AAATTAATTT TAGAAATATG ATTTATGCCT TTTGTTGAAT	4677
CATTAACATA TATACAGAAA CAGTTAAAAC AACCACAGCA TAAGAGAAAA ACTTCTAGAA	4737
TGGATATGCT GTATTCATCA GTGTGTTCTT TAAATTATAG GG AAG GCC AAA AAT Arg Lys Ala Lys Asn 180	4791
CCC CCT GGA GAC TCC AGC CTA CAC TGG CCA GCC ATG GCA TTG CCA GCA Pro Pro Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala 185 190 195	4839
TTG TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys 200 205 210	4887
GTAAGTGGTA CCATTCCTTT TTTTAAAAAT ATGCTATGTT TACATAAATT ATCATCTTTT	4947
TTTCCTCAAG AAATGATCCT TTAAGAAAAC AGTGAATCTA CCTTAGCTTA TACTAAACAA	5007
AATTTAAATT TTATAAAGTT TCCTGTTTCT CATTATGTCT GGAGACAATC CCTCTAGCTG	5067
ATAATTCACG CTTAAGAATT AGGAACTAAA ACTGTTATTG GAGTTATTGC CATAAAAGAT	5127
AAAAGTGGAG TCCACTTACC TCTTAAATAT TAGACCATTC ATTGATTATT TTACAGTATA	5187
TGTCTTTCTT CTTTTTCCAG AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT Lys Arg Gln Pro Ser Leu Thr Arg Ala Val 215 220	5237
GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA AG GTATTTTGTT Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser 225 230 235	5285
TTGCTAAATG TGTGCCCAAT CAAGCATGAC ATTGCCATTT CACACACTGT GTACCTGCCC	5345
ATAATGTCTT TAAGAAGTCC TTTACTCATG ACAGTAGCTC CTAACCAAGTG AGTCCCAACT	5405
CTATCCATGT TTCTGATGTC TCACTCTCTC TTCGTATGTG TATATGCATA TACAGAGAAA	5465
GAAATGTTTT AACTACTTGG AAAGACTACC TTAAGACAAA TGAAGTCTTC CCTCTTCCCT	5525
ATAGTAATAA GAAGGTAGGC TCCCCCATTC AATTTTGCAA TCTTCTGCTA CTATATTTAC	5585
AGAAAAGCTG CCTTTTACAA TGCCGAGATC ATGGTGTACC TCAGAATCTC TGACCAAGAG	5645
CAAATAAGCA TTTTTTCTTA TTGTTTTTCA G T ATG TTG CAA GAG AAA GAG AGA Met Leu Gln Glu Lys Glu Arg 240	5698
GAG TTT CAA GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG Glu Phe Gln Glu Val 245	5753

GTAAGTTTTT TTCTTCTTTC CTTTTTTTTT CTTTTTTTTA TTATACTTTA AGTTCTAGGG 5813  
TACATGTGCA CAATGTGCAG GTTTGTTACG TATGTTTACA TGTGCCATGT T 5864

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
-25 -20 -15 -10  
Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
-5 1 5  
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
10 15 20  
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
25 30 35  
Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
40 45 50 55  
Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
60 65 70  
Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
75 80 85  
Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
90 95 100  
Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
105 110 115  
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr  
120 125 130 135  
Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg  
140 145 150  
Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
155 160 165  
Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro  
170 175 180  
Gly Asp Ser Ser Leu His Trp Pro Ala Met Ala Leu Pro Ala Leu Phe  
185 190 195  
Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg  
200 205 210 215  
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
220 225 230

Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
 235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 273 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	1	5	10	15
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	20	25	30	
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	35	40	45	
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	50	55	60	
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	65	70	75	80
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	85	90	95	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	100	105	110	
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	115	120	125	
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	130	135	140	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	145	150	155	160
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	165	170	175	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	180	185	190	
Leu	Arg	Asn	Asp	Ser	Ser	Ser	Ser	Asn	Arg	Lys	Ala	Lys	Asn	Pro	Pro	195	200	205	
Gly	Asp	Ser	Ser	Leu	His	Trp	Ala	Ala	Met	Ala	Leu	Pro	Ala	Leu	Phe	210	215	220	
Ser	Leu	Ile	Ile	Gly	Phe	Ala	Phe	Gly	Ala	Leu	Tyr	Trp	Lys	Lys	Arg	225	230	235	240

Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
245 250 255  
Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
260 265 270  
Val

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
1 5 10 15  
Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
20 25 30  
Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
35 40 45  
Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
50 55 60  
Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
65 70 75 80  
Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
85 90 95  
Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
100 105 110  
Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
115 120 125  
Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
130 135 140  
Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Ala Val Ala Ser Glu Thr  
145 150 155 160  
Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg  
165 170 175  
Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
180 185 190  
Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Thr  
195 200 205  
Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Phe Phe  
210 215 220

Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg  
 225 230 235 240  
 Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 245 250 255  
 Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
 260 265 270  
 Val

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 274 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu  
 1 5 10 15  
 Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Gly Ile Cys Gly Lys Arg  
 20 25 30  
 Val Thr Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
 35 40 45  
 Lys Asp Tyr Lys Ile Ala Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
 50 55 60  
 Pro Ser His Cys Trp Ile Ser Val Met Val Glu Gln Leu Ser Val Ser  
 65 70 75 80  
 Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
 85 90 95  
 Asn Tyr Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val  
 100 105 110  
 Glu Cys Thr Glu Gly Tyr Ser Phe Glu Asn Val Lys Lys Ala Pro Lys  
 115 120 125  
 Ser Pro Glu Leu Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
 130 135 140  
 Asn Arg Ser Ile Asp Ala Phe Lys Asp Leu Glu Thr Val Ala Ser Lys  
 145 150 155 160  
 Ser Ser Glu Cys Val Val Ser Ser Thr Leu Ser Pro Asp Lys Asp Ser  
 165 170 175  
 Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser  
 180 185 190  
 Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser  
 195 200 205

Ile Gly Asp Ser Asn Leu Gln Trp Ala Ala Met Ala Leu Pro Ala Phe  
 210 215 220

Phe Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys  
 225 230 235 240

Lys Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Ile Gln Ile Asn Glu  
 245 250 255

Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln  
 260 265 270

Glu Val

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Thr Gln Thr Trp Ile Val Thr Cys Ile Tyr Leu Gln Leu Leu  
 1 5 10 15

Phe Asn Pro Leu Val Lys Thr Lys Gly Leu Cys Arg Asn Arg Val Thr  
 20 25 30

Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp  
 35 40 45

Tyr Lys Ile Ala Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser  
 50 55 60

His Cys Trp Ile Ser Val Met Val Glu Gln Leu Ser Val Ser Leu Thr  
 65 70 75 80

Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr  
 85 90 95

Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val Glu Cys  
 100 105 110

Val Glu Gly His Ser Ser Glu Asn Val Lys Lys Ser Ser Lys Ser Pro  
 115 120 125

Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg  
 130 135 140

Ser Ile Asp Ala Phe Lys Asp Leu Glu Met Val Ala Ser Lys Thr Ser  
 145 150 155 160

Glu Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val  
 165 170 175

Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu  
 180 185 190



Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Thr Asn Pro Ile Glu Asp  
195 200 205

Ser Ser Ile Gln Trp Ala Val Met Ala Leu Pro Ala Cys Phe Ser Leu  
210 215 220

Val Ile Gly Phe Ala Phe Gly Ala Phe Tyr Trp Lys Lys Lys Gln Pro  
225 230 235 240

Asn Leu Thr Arg Thr Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn  
245 250 255

Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu Val  
260 265 270

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu  
1 5 10 15

Leu Leu Phe Asn Pro Leu Val His Thr Gln Gly Ile Cys Ser Asn Arg  
20 25 30

Val Thr Asp Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
35 40 45

Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
50 55 60

Pro Ser His Cys Trp Ile Ser Glu Met Val Glu Gln Leu Ser Val Ser  
65 70 75 80

Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
85 90 95

Asn Tyr Cys Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val  
100 105 110

Glu Cys Met Glu His Ser Ser Glu Asn Val Lys Lys Ser Ser Lys Ser  
115 120 125

Pro Glu Pro Arg Gln Phe Thr Pro Glu Lys Phe Phe Gly Ile Phe Asn  
130 135 140

Lys Ser Ile Asp Ala Phe Lys Asp Leu Glu Ile Val Ala Ser Lys Met  
145 150 155 160

Ser Glu Cys Val Ile Ser Ser Thr Ser Ser Pro Glu Lys Asp Ser Arg  
165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
180 185 190

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ser Asn Ser Ile  
 195 200 205  
 Glu Asp Ser Ser Leu Gln Trp Ala Ala Val Ala Leu Pro Ala Phe Phe  
 210 215 220  
 Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Phe Tyr Trp Lys Lys Lys  
 225 230 235 240  
 Gln Pro Asn Leu Thr Arg Thr Val Glu Asn Arg Gln Ile Asn Glu Glu  
 245 250 255  
 Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
 260 265 270  
 Val

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu  
 1 5 10 15  
 Leu Leu Phe Asn Pro Leu Val Lys Thr Gln Glu Ile Cys Arg Asn Pro  
 20 25 30  
 Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro  
 35 40 45  
 Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu  
 50 55 60  
 Pro Ser His Cys Trp Leu Arg Asp Met Val Thr His Leu Ser Val Ser  
 65 70 75 80  
 Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
 85 90 95  
 Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val  
 100 105 110  
 Ala Cys Met Glu Glu Asn Ala Pro Leu Asn Val Lys Glu Ser Leu Lys  
 115 120 125  
 Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe  
 130 135 140  
 Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr  
 145 150 155 160  
 Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg  
 165 170 175

Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
 180 185 190  
 Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ser Pro  
 195 200 205  
 Glu Asp Pro Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile  
 210 215 220  
 Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys  
 225 230 235 240  
 Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 245 250 255  
 Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
 260 265 270  
 Val

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu  
 1 5 10 15  
 Leu Leu Phe Asn Pro Leu Val Lys Thr Lys Glu Ile Cys Gly Asn Pro  
 20 25 30  
 Val Thr Asp Asn Val Lys Asp Ile Thr Lys Leu Val Ala Asn Leu Pro  
 35 40 45  
 Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val Ala Gly Met Asp Val Leu  
 50 55 60  
 Pro Ser His Cys Trp Leu Arg Asp Met Val Ile Gln Leu Ser Leu Ser  
 65 70 75 80  
 Leu Thr Thr Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
 85 90 95  
 Asn Tyr Ser Ile Ile Asp Lys Leu Gly Lys Ile Val Asp Asp Leu Val  
 100 105 110  
 Leu Cys Met Glu Glu Asn Ala Pro Lys Asn Ile Lys Glu Ser Pro Lys  
 115 120 125  
 Arg Pro Glu Thr Arg Ser Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe  
 130 135 140  
 Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr  
 145 150 155 160

Ser Asp Cys Val Leu Ser Ser Thr Leu Gly Pro Glu Lys Asp Ser Arg  
 165 170 175  
 Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser  
 180 185 190  
 Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Ala Lys Ala Pro  
 195 200 205  
 Glu Asp Ser Gly Leu Gln Trp Thr Ala Met Ala Leu Pro Ala Leu Ile  
 210 215 220  
 Ser Leu Val Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Lys  
 225 230 235 240  
 Gln Ser Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 245 250 255  
 Asp Asn Glu Ile Ser Met Leu Gln Gln Lys Glu Arg Glu Phe Gln Glu  
 260 265 270

Val

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Thr Trp Ile Ile Thr Cys Phe Cys Leu Gln Leu Leu Leu Leu Asn Pro  
 1 5 10 15  
 Leu Val Lys Ala Gln Ser Ser Cys Gly Asn Pro Val Thr Asp Asp Val  
 20 25 30  
 Asn Asp Ile Ala Lys Leu Val Gly Asn Leu Pro Asn Asp Tyr Leu Ile  
 35 40 45  
 Thr Leu Lys Tyr Val Pro Lys Met Asp Ser Leu Pro Asn His Cys Trp  
 50 55 60  
 Leu His Leu Met Val Pro Glu Phe Ser Arg Ser Leu His Asn Leu Leu  
 65 70 75 80  
 Gln Lys Phe Ser Asp Ile Ser Asp Met Ser Asp Val Leu Ser Asn Tyr  
 85 90 95  
 Ser Ile Ile Asn Asn Leu Thr Arg Ile Ile Asn Asp Leu Met Ala Cys  
 100 105 110  
 Leu Ala Phe Asp Lys Asn Lys Asp Phe Ile Lys Glu Asn Gly Leu His  
 115 120 125  
 Tyr Glu Glu Asp Arg Phe Ile Pro Glu Asn Phe Phe Arg Leu Phe Asn  
 130 135 140

Ser Thr Ile Glu Val Tyr Lys Glu Phe Ala Asp Ser Leu Asp Lys Asn  
 145 150 155 160  
 Asp Cys Ile Met Pro Ser Thr Val Glu Thr Pro Glu Asn Asp Ser Arg  
 165 170 175  
 Val Ala Val Thr Lys Thr Ile Ser Phe Pro Pro Val Ala Ala Ser Ser  
 180 185 190  
 Leu Arg Asn Asp Ser Ile Gly Ser Asn Thr Ser Ser Asn Ser Asn Lys  
 195 200 205  
 Glu Ala Leu Gly Phe Ile Ser Ser Ser Ser Leu Gln Gly Ile Ser Ile  
 210 215 220  
 Ala Leu Thr Ser Leu Leu Ser Leu Leu Ile Gly Phe Ile Leu Gly Ala  
 225 230 235 240  
 Ile Tyr Trp Lys Lys Thr His Pro Lys Ser Arg Pro Glu Ser Asn Glu  
 245 250 255  
 Thr Ile Gln Cys His Gly Cys Gln Glu Glu Asn Glu Ile Ser Met Leu  
 260 265 270  
 Gln Gln Lys Glu Lys Glu His Leu Gln Val  
 275 280

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Lys Lys Thr Gln Thr Trp Ile Ile Thr Cys Ile Tyr Leu Gln Leu  
 1 5 10 15  
 Leu Leu Phe Asn Pro Leu Val Lys Thr Gly Ile Cys Arg Asn Arg Val  
 20 25 30  
 Thr Asp Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro Lys Asp  
 35 40 45  
 Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu Pro Ser  
 50 55 60  
 His Cys Trp Ile Ser Glu Met Val Glu Gln Leu Ser Val Ser Leu Thr  
 65 70 75 80  
 Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr  
 85 90 95  
 Ser Ile Ile Asp Lys Leu Val Lys Ile Val Asp Asp Leu Val Glu Cys  
 100 105 110  
 Glu Glu Asn Ser Ser Lys Asn Val Lys Lys Ser Lys Ser Pro Glu Pro  
 115 120 125

Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile  
 130 135 140  
 Asp Ala Phe Lys Asp Phe Met Val Ala Ser Lys Thr Ser Asp Cys Val  
 145 150 155 160  
 Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr  
 165 170 175  
 Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn Asp  
 180 185 190  
 Ser Ser Ser Ser Asn Arg Lys Ala Asn Glu Asp Ser Ser Leu Gln Trp  
 195 200 205  
 Ala Ala Met Ala Leu Pro Ala Leu Phe Ser Leu Val Ile Gly Phe Ala  
 210 215 220  
 Phe Gly Ala Leu Tyr Trp Lys Lys Lys Gln Pro Ser Leu Thr Arg Ala  
 225 230 235 240  
 Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu  
 245 250 255  
 Gln Glu Lys Glu Arg Glu Phe Gln Glu Val  
 260 265

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 269 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(1..210, 223..258)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAA TTC TTC CGT ATC TTC AAC CGT TCC ATC GAC GCT TTC AAA GAC TTC	48
Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe	
1 5 10 15	
GTT GTT GCT TCC GAA ACC TCC GAC TGC GTT GTT TCC TCC ACC CTG TCT	96
Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser	
20 25 30	
CCG GAA AAA GAC TCC CGT GTT TCG GTT ACC AAA CCG TTC ATG CTG CCG	144
Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro	
35 40 45	
CCG GTT GCT GCT TCC TCC CTG CGT AAC GAC TCC TCC TCC TCC AAC TCC	192
Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser	
50 55 60	
AAA TAC ATC TAC CTG ATC TAATAGGATC CG GTT ACC AAA CCG TTC ATG	240
Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met	
65 70 75	

CTG CCG CCG GTT GCT GCT TAATAGGATC C  
 Leu Pro Pro Val Ala Ala  
 80

269

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 82 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe  
 1 5 10 15  
 Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser  
 20 25 30  
 Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro  
 35 40 45  
 Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Ser  
 50 55 60  
 Lys Tyr Ile Tyr Leu Ile Val Thr Lys Pro Phe Met Leu Pro Pro Val  
 65 70 75 80  
 Ala Ala

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1404 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 184..1002

- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 259..1002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCGCCTCGCG CCGAGACTAG AAGCGCTGCG GGAAGCAGGG ACAGTGGAGA GGGCGCTGCG 60  
 CTCGGGCTAC CCAATGCGTG GACTATCTGC CGCCGCTGTT CGTGCAATAT GCTGGAGCTC 120  
 CAGAACAGCT AAACGGAGTC GCCACACCAC TGTTTGTGCT GGATCGCAGC GCTGCCTTTC 180  
 CTT ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG 228  
 Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln  
 -25 -20 -15

CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG AAT Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn -10 -5 1 5	276
CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA AAT CTT Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu 10 15 20	324
CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG ATG GAT GTT Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val 25 30 35	372
TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA CAA TTG TCA GAC Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp 40 45 50	420
AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT ATT TCT GAA GGC TTG Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu 55 60 65 70	468
AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG AAT ATA GTG GAT GAC CTT Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu 75 80 85	516
GTG GAG TGC GTG AAA GAA AAC TCA TCT AAG GAT CTA AAA AAA TCA TTC Val Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe 90 95 100	564
AAG AGC CCA GAA CCC AGG CTC TTT ACT CCT GAA GAA TTC TTT AGA ATT Lys Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile 105 110 115	612
TTT AAT AGA TCC ATT GAT GCC TTC AAG GAC TTT GTA GTG GCA TCT GAA Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu 120 125 130	660
ACT AGT GAT TGT GTG GTT TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC Thr Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser 135 140 145 150	708
AGA GTC AGT GTC ACA AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser 155 160 165	756
TCC CTT AGG AAT GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro 170 175 180	804
CCT GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu 185 190 195	852
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys 200 205 210	900
AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu 215 220 225 230	948
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln 235 240 245	996



GAA GTG TAATTGTGGC TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA 1052  
Glu Val

GTTTCATGTTT GCTTCATAAA TGAAGCAGCT TTAACAAAT TCATATTCTG TCTGGAGTGA 1112  
CAGACCACAT CTTTATCTGT TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG 1172  
GAACAGAATG TTTTACTGTG AACTGGCAC TGAATTAATC ATCTATAAAG AAGAACTTGC 1232  
ATGGAGCAGG ACTCTATTTT AAGGACTGCG GGACTTGGGT CTCATTTAGA ACTTGCAGCT 1292  
GATGTTGGAA GAGAAAGCAC GTGTCTCAGA CTGCATGTAC CATTTGCATG GCTCCAGAAA 1352  
TGTCTAAATG CTGAAAAAAC ACCTAGCTTT ATTCTTCAGA TACAACTGC AG 1404

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met	Lys	Lys	Thr	Gln	Thr	Trp	Ile	Leu	Thr	Cys	Ile	Tyr	Leu	Gln	Leu	-25	-20	-15	-10
Leu	Leu	Phe	Asn	Pro	Leu	Val	Lys	Thr	Glu	Gly	Ile	Cys	Arg	Asn	Arg	-5	1	5	
Val	Thr	Asn	Asn	Val	Lys	Asp	Val	Thr	Lys	Leu	Val	Ala	Asn	Leu	Pro	10	15	20	
Lys	Asp	Tyr	Met	Ile	Thr	Leu	Lys	Tyr	Val	Pro	Gly	Met	Asp	Val	Leu	25	30	35	
Pro	Ser	His	Cys	Trp	Ile	Ser	Glu	Met	Val	Val	Gln	Leu	Ser	Asp	Ser	40	45	50	55
Leu	Thr	Asp	Leu	Leu	Asp	Lys	Phe	Ser	Asn	Ile	Ser	Glu	Gly	Leu	Ser	60	65	70	
Asn	Tyr	Ser	Ile	Ile	Asp	Lys	Leu	Val	Asn	Ile	Val	Asp	Asp	Leu	Val	75	80	85	
Glu	Cys	Val	Lys	Glu	Asn	Ser	Ser	Lys	Asp	Leu	Lys	Lys	Ser	Phe	Lys	90	95	100	
Ser	Pro	Glu	Pro	Arg	Leu	Phe	Thr	Pro	Glu	Glu	Phe	Phe	Arg	Ile	Phe	105	110	115	
Asn	Arg	Ser	Ile	Asp	Ala	Phe	Lys	Asp	Phe	Val	Val	Ala	Ser	Glu	Thr	120	125	130	135
Ser	Asp	Cys	Val	Val	Ser	Ser	Thr	Leu	Ser	Pro	Glu	Lys	Asp	Ser	Arg	140	145	150	
Val	Ser	Val	Thr	Lys	Pro	Phe	Met	Leu	Pro	Pro	Val	Ala	Ala	Ser	Ser	155	160	165	

Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro  
 170 175 180  
 Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe  
 185 190 195  
 Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg  
 200 205 210 215  
 Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu  
 220 225 230  
 Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu  
 235 240 245

Val

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 151..885

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 226..885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCAGGGACA GTGGAGAGGG CGCTGCGCTC GGGCTACCCA ATGCGTGGAC TATCTGCCGC 60  
 CGCTGTTCGT GCAATATGCT GGAGCTCCAG AACAGCTAAA CGGAGTCGCC ACACCACTGT 120  
 TTGTGCTGGA TCGCAGCGCT GCCTTTCCTT ATG AAG AAG ACA CAA ACT TGG ATT 174  
 Met Lys Lys Thr Gln Thr Trp Ile  
 -25 -20  
 CTC ACT TGC ATT TAT CTT CAG CTG CTC CTA TTT AAT CCT CTC GTC AAA 222  
 Leu Thr Cys Ile Tyr Leu Gln Leu Leu Leu Phe Asn Pro Leu Val Lys  
 -15 -10 -5  
 ACT GAA GGG ATC TGC AGG AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC 270  
 Thr Glu Gly Ile Cys Arg Asn Arg Val Thr Asn Asn Val Lys Asp Val  
 1 5 10 15  
 ACT AAA TTG GTG GCA AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA 318  
 Thr Lys Leu Val Ala Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys  
 20 25 30  
 TAT GTC CCC GGG ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG 366  
 Tyr Val Pro Gly Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu  
 35 40 45

ATG GTA GTA CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT Met Val Val Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe 50 55 60	414
TCA AAT ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu 65 70 75	462
GTG AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT Val Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser 80 85 90 95	510
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT ACT Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe Thr 100 105 110	558
CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC TTC AAG Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys 115 120 125	606
GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT TCT TCA ACA Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val Ser Ser Thr 130 135 140	654
TTA AGT CCT GAG AAA GGG AAG GCC AAA AAT CCC CCT GGA GAC TCC AGC Leu Ser Pro Glu Lys Gly Lys Ala Lys Asn Pro Pro Gly Asp Ser Ser 145 150 155	702
CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT CTT ATA ATT Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser Leu Ile Ile 160 165 170 175	750
GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA CAG CCA AGT CTT Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg Gln Pro Ser Leu 180 185 190	798
ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA GAG GAT AAT GAG ATA Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu Glu Asp Asn Glu Ile 195 200 205	846
AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT CAA GAA GTG TAATTGTGGC Ser Met Leu Gln Glu Lys Glu Arg Glu Phe Gln Glu Val 210 215 220	895
TTGTATCAAC ACTGTTACTT TCGTACATTG GCTGGTAACA GTTCATGTTT GCTTCATAAA	955
TGAAGCAGCT TTAACAAAT TCATATTCTG TCTGGAGTGA CAGACCACAT CTTTATCTGT	1015
TCTTGCTACC CATGACTTTA TATGGATGAT TCAGAAATTG GAACAGAATG TTTTACTGTG	1075
AAACTGGCAC TGA	1088

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln Leu  
 -25 -20 -15 -10  
 Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg Asn Arg  
 -5 1 5  
 Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala Asn Leu Pro  
 10 15 20  
 Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly Met Asp Val Leu  
 25 30 35  
 Pro Ser His Cys Trp Ile Ser Glu Met Val Val Gln Leu Ser Asp Ser  
 40 45 50 55  
 Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser  
 60 65 70  
 Asn Tyr Ser Ile Ile Asp Lys Leu Val Asn Ile Val Asp Asp Leu Val  
 75 80 85  
 Glu Cys Val Lys Glu Asn Ser Ser Lys Asp Leu Lys Lys Ser Phe Lys  
 90 95 100  
 Ser Pro Glu Pro Arg Leu Phe Thr Pro Glu Glu Phe Phe Arg Ile Phe  
 105 110 115  
 Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Val Val Ala Ser Glu Thr  
 120 125 130 135  
 Ser Asp Cys Val Val Ser Ser Thr Leu Ser Pro Glu Lys Gly Lys Ala  
 140 145 150  
 Lys Asn Pro Pro Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu  
 155 160 165  
 Pro Ala Leu Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr  
 170 175 180  
 Trp Lys Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln  
 185 190 195  
 Ile Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg  
 200 205 210 215  
 Glu Phe Gln Glu Val  
 220

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Glu Glu Ile Cys Arg Asn Pro Val Thr Asp Asn Val Lys Asp Ile Thr  
 1 5 10 15

Lys Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr  
20 25 30

Val Ala Gly Met Asp Val Leu Pro Ser His Xaa Trp Leu Arg Asp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ile Thr Thr Leu Asn Tyr Val Ala Gly Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Ala Ser Asp Thr Ser Asp Cys Val Leu Ser Xaa Xaa Leu Gly Pro  
1 5 10 15

Glu Lys Asp Ser Arg Val Ser Val Xaa Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp Val Leu Pro Ser His Cys Trp Leu Arg Asp Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Glu Glu Asn Ala Pro Lys Asn Val Glu Ser Leu Lys Lys Pro Thr Arg  
1 5 10 15

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Asp Arg Ser Ile Asp  
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Glu Ser Leu Lys Lys Pro Glu Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Val Ser Val Xaa Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ile Val Asp Asp Leu Val Ala Ala Met Glu Glu Asn Ala Pro Lys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn Phe Thr Pro Glu Glu Phe Phe Ser Ile Phe Xaa Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Val Ala Asn Leu Pro Asn Asp Tyr Met Ile Thr Leu Asn Tyr Val  
1 5 10 15

Ala Gly Asp Asp Val Leu Pro Ser His Cys Trp Leu Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala Ser Asp Thr Ser Asp  
1 5 10 15

Cys Val Leu Ser Xaa Xaa Leu Gly  
20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe  
1 5 10 15

Phe Ser Ile Phe Xaa Arg  
20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Glu Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe  
 1 5 10 15  
  
Phe Ser Ile Phe Asp Arg  
 20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Asn Ala Pro Lys Asn Val Lys Glu  
 1 5

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Arg Val Ser Val Xaa Lys Pro Phe Met Leu Pro Pro Val Ala Ala  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 34 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe  
 1 5 10 15  
  
Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala  
 20 25 30



Ser Asp

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Leu Lys Lys Pro Glu Thr Arg Asn Phe Thr Pro Glu Glu Phe Phe  
1 5 10 15  
Ser Ile Phe Asn Arg Ser Ile Asp Ala Phe Lys Asp Phe Met Val Ala  
20 25 30  
Ser Asp Thr Ser Asp  
35

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu Arg Asp Met Val Thr His Leu Ser Val Ser Leu Thr Thr Leu Leu  
1 5 10 15  
Asp Lys Phe Ser Asn Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile  
20 25 30  
Asp Lys Leu Gly Lys Ile Val Asp  
35 40

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala Ala  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Pro Val Ala Ala  
1

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CCTGAGAAAG ATTCCAGAGTC

21

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTGCAGTTTG TATCTGAAG

19

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CATATAAAGT CATGGGTAG

19

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:  
 ACTTGTGTCT TCTTCATAAG GAAAGCC 27

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:  
 TGTACGAAAG TAACAGTGTT G 21

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:  
 ACTGCTCCTA TTTAATCCTC TC 22

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:  
 CACTGACTCT GGAATCTTTC TCA 23

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:  
 TCGACCCGGA TCCCC 15

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TCGAGGGGAT CCGGG

15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TCTTCTTCAT GCGGCGGCA AGCTT

25

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Ser	Arg	Val	Ser	Val	Xaa	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5				10					15		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Asp	Ser	Arg	Val	Ser	Val	Thr	Lys	Pro	Phe	Phe	Met	Leu	Pro	Pro	Val
1				5				10					15		

Ala Ala

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 55 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GGTAC

55

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT

49

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAGGA

9

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATCTCCTGC A

11

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGGAAGGT ATCTGCA

17

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GATACCTTCC A

11

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTCCTTATG

10

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCCGCCGCCA TG

12

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TCTTCTTCAT GCGGCGGCA AGCTT

25